Claims: -

1. A method for characterising nucleic acid molecules, which comprises the steps of:

i) introducing a modified base which is a substrate for a DNA endonuclease into a target DNA molecule; and

ii) reacting the nucleic acid containing the modified base with said DNA endonuclease such that the nucleic acid is cleaved to generate an upstream fragment containing said modified base and bearing a 3' hydroxyl group.

2. A method according to Claim 1, wherein the modified base is introduced by enzymatic amplification of the nucleic acid.

3. A method according to Claim 1 or 2, wherein a nucleotide containing the modified base partially replaces a normal precursor nucleotide.

4. A method according to Claim 1 or 2, wherein a nucleotide containing the modified base totally replaces a normal precursor nucleotide.

5. A method according to Claim 1, wherein the modified base is introduced by chemical modification of an existing base.

6. A method according to any preceding claim, wherein the modified base is selected from inosine and uracil.

7. A method according to any preceding claim, wherein the endonuclease is a thermostable endonuclease.

8. A method according to any preceding claim, wherein the endonuclease cleavage reaction is carried out concurrently with a thermocycled amplification reaction using a thermostable endonuclease.

9. A method according to any one of Claims 2-8, wherein at least one of the primers for the amplification step is positioned adjacent a locus where a DNA sequence variation occurs.

10. A method according to any one of Claims 1-6 and 9, wherein the endonuclease is Endonuclease V from *E. coli*.

11. A method according to any preceding claim, wherein the upstream fragment generated in step ii) is used as a primer for a subsequent extension reaction.

12. A method according to Claim 11, wherein the extension is carried out using a DNA polymerase.

13. A method according to Claim 11, wherein the extension is carried out using a DNA ligase.

14. A method according to Claim 1, substantially as herein before described and exemplified

15. A method according to any preceding claim for use in detecting polymorphisms and mutations.

16. A method according to any one of Claims 1-14, for use in nucleic acid identification and profiling.

17. A method according to any one of Claims 1-14, for rapidly genotyping known polymorphisms and mutations.

18. A method according to any one of Claims 1-14, for scanning a nucleic acid sequence for the presence of known or unknown mutations and polymorphisms.